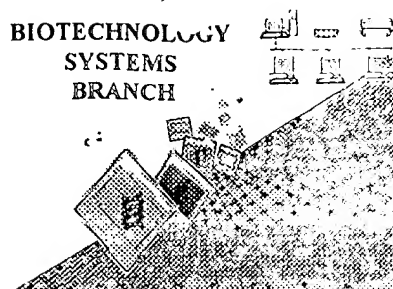


RAW SEQUENCE LISTING **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/654,281

Source: 1642

Date Processed by STIC: 3/16/2001

BEST AVAILABLE COPY

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/654,281

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☒ Variable Length Sequence(s) 1 contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☒ Use of <213>Organism (NEW RULES) Sequence(s) ____ are missing this mandatory field or its response.
- 12 ☒ Use of <220>Feature (NEW RULES) Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted "file," resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

1642

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/654,281

DATE: 03/16/2001
TIME: 15:13:59

Input Set : A:\PTO.txt
Output Set: N:\CRF3\03162001\I654281.raw

Does Not Comply
Corrected Diskette Needed

pp 1-2, 5

3 <110> APPLICANT: Sedivy, John
4 Kolch, Walter
5 Yeung, Kam Chi
7 <120> TITLE OF INVENTION: Kinase Inhibitors and Methods of Use in Screening Assays and Modulation
8 of Cell Proliferation and Growth
10 <130> FILE REFERENCE: 3564/1010
12 <140> CURRENT APPLICATION NUMBER: 09/654,281
13 <141> CURRENT FILING DATE: 2000-09-01
15 <150> PRIOR APPLICATION NUMBER: 60/151,992
16 <151> PRIOR FILING DATE: 1999-09-01
18 <160> NUMBER OF SEQ ID NOS: 11
20 <170> SOFTWARE: PatentIn version 3.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 42
24 <212> TYPE: PRT
25 <213> ORGANISM: Artificial/Unknown
27 <220> FEATURE:
28 <221> NAME/KEY: UNSURE
29 <222> LOCATION: (3)..(5) Xaa
30 <223> OTHER INFORMATION: X = any amino acid
33 <220> FEATURE:
34 <221> NAME/KEY: UNSURE
35 <222> LOCATION: (9)..(9) delete
36 <223> OTHER INFORMATION: Z = a hydrophobic amino acid residue
39 <220> FEATURE:
40 <221> NAME/KEY: UNSURE
41 <222> LOCATION: (11)..(13) Xaa
42 <223> OTHER INFORMATION: X = any amino acid
45 <220> FEATURE:
46 <221> NAME/KEY: UNSURE
47 <222> LOCATION: (14)..(14) delete
48 <223> OTHER INFORMATION: B = a negatively charged amino acid residue
51 <220> FEATURE:
52 <221> NAME/KEY: UNSURE
53 <222> LOCATION: (15)..(18) Xaa
54 <223> OTHER INFORMATION: X = any amino acid residue
57 <220> FEATURE:
58 <221> NAME/KEY: UNSURE
59 <222> LOCATION: (20)..(21) Xaa
60 <223> OTHER INFORMATION: X = any amino acid residue
63 <220> FEATURE:
64 <221> NAME/KEY: UNSURE
65 <222> LOCATION: (23)..(23) Xaa
66 <223> OTHER INFORMATION: X = between 10 and 50 of any amino acid residue
69 <220> FEATURE:
70 <221> NAME/KEY: UNSURE
71 <222> LOCATION: (25)..(28)

please correct this error if appearing in subsequent sequences
invalid - per 1.823 of new Sequence Rules, the only valid <213> responses are:
Unknown or Artificial Sequence
or scientific name
(Genus/species)
(one of the three)

also,
see item 12
on Error
Summary Sheet

variable length
not permitted - see
item 6 on Error
Summary Sheet

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/654,281

DATE: 03/16/2001
TIME: 15:13:59

Input Set : A:\PTO.txt
Output Set: N:\CRF3\03162001\I654281.raw

72 <223> OTHER INFORMATION: ^{Xaa}(X) = any amino acid residue
75 <220> FEATURE:
76 <221> NAME/KEY: UNSURE
77 <222> LOCATION: (30)..(30) ^{Xaa}
78 <223> OTHER INFORMATION: (X) = between 2 and 4 of any amino acid residue
81 <220> FEATURE:
82 <221> NAME/KEY: UNSURE
83 <222> LOCATION: (32)..(32) ^{Xaa}
84 <223> OTHER INFORMATION: (X) = any amino acid residue
87 <220> FEATURE:
88 <221> NAME/KEY: UNSURE
89 <222> LOCATION: (35)..(35) ^{Xaa}
90 <223> OTHER INFORMATION: (X) = an aromatic amino acid residue
93 <220> FEATURE:
94 <221> NAME/KEY: UNSURE
95 <222> LOCATION: (37)..(37) ^{Xaa}
96 <223> OTHER INFORMATION: (X) = any amino acid residue
99 <220> FEATURE:
100 <221> NAME/KEY: UNSURE
101 <222> LOCATION: (38)..(38) ^{delete}
102 <223> OTHER INFORMATION: (X) = a hydrophobic amino acid residue
105 <220> FEATURE:
106 <221> NAME/KEY: UNSURE
107 <222> LOCATION: (39)..(41) ^{Xaa}
108 <223> OTHER INFORMATION: (X) = any amino acid residue
111 <400> SEQUENCE: 1
W--> 113 Thr Leu Xaa Xaa Xaa Asp Pro Asp Glx Pro Xaa Xaa Xaa Asx Xaa Xaa
114 1 5 10 15
W--> 116 Xaa Xaa Glu Xaa Xaa His Xaa Tyr Xaa Xaa Xaa Xaa Pro Xaa Gly Xaa
117 20 25 30
W--> 119 His Arg Xaa Val Xaa Glx Xaa Xaa Xaa Gln
120 35 40
122 <210> SEQ ID NO: 2
123 <211> LENGTH: 187
124 <212> TYPE: PRT
125 <213> ORGANISM: Homo sapiens
127 <400> SEQUENCE: 2
129 Met Pro Val Asp Leu Ser Lys Trp Ser Gly Pro Leu Ser Leu Gln Glu
130 1 5 10 15
132 Val Asp Glu Gln Pro Gln His Pro Leu His Val Thr Tyr Ala Gly Ala
133 20 25 30
135 Ala Val Asp Glu Leu Gly Lys Val Leu Thr Pro Thr Gln Val Lys Asn
136 35 40 45
138 Arg Pro Thr Ser Ile Ser Trp Asp Gly Leu Asp Ser Gly Lys Leu Tyr
139 50 55 60
141 Thr Leu Val Leu Thr Asp Pro Asp Ala Pro Ser Arg Lys Asp Pro Lys
142 65 70 75 80
144 Tyr Arg Glu Trp His His Phe Leu Val Val Asn Met Lys Gly Asn Asp
145 85 90 95

see item 6 on Error Summary sheet

RAW SEQUENCE LISTING DATE: 03/16/2001
 PATENT APPLICATION: US/09/654,281 TIME: 15:13:59

Input Set : A:\PTO.txt
 Output Set: N:\CRF3\03162001\I654281.raw

```

147 Ile Ser Ser Gly Thr Val Leu Ser Asp Tyr Val Gly Ser Gly Pro Pro
148           100           105           110
150 Lys Gly Thr Gly Leu His Arg Tyr Val Trp Leu Val Tyr Glu Gln Asp
151           115           120           125
153 Arg Pro Leu Lys Cys Asp Glu Pro Ile Leu Ser Asn Arg Ser Gly Lys
154           130           135           140
156 His Arg Gly Lys Phe Lys Val Ala Ser Phe Arg Lys Lys Tyr Glu Leu
157 145           150           155           160
159 Arg Ala Pro Val Ala Gly Thr Cys Tyr Gln Ala Glu Trp Lys Lys Tyr
160           165           170           175
162 Val Pro Lys Leu Tyr Glu Gln Leu Ser Gly Lys
163           180           185
165 <210> SEQ ID NO: 3
166 <211> LENGTH: 187
167 <212> TYPE: PRT
168 <213> ORGANISM: Mus musculus
170 <220> FEATURE:
171 <221> NAME/KEY: UNSURE
172 <222> LOCATION: (150)..(150)
173 <223> OTHER INFORMATION: X = any amino acid residue
176 <400> SEQUENCE: 3
178 Met Ala Ala Asp Ile Ser Gln Trp Ala Gly Pro Leu Cys Leu Gln Glu
179 1           5           10           15
181 Val Asp Glu Pro Pro Gln His Ala Leu Arg Val Asp Tyr Ala Gly Val
182           20           25           30
184 Thr Val Asp Glu Leu Gly Lys Val Leu Thr Pro Thr Gln Val Met Asn
185           35           40           45
187 Arg Pro Ser Ser Ile Ser Trp Asp Gly Leu Asp Pro Gly Lys Leu Tyr
188           50           55           60
190 Thr Leu Val Leu Thr Asp Pro Asp Ala Pro Ser Arg Lys Asp Pro Lys
191 65           70           75           80
193 Phe Arg Glu Trp His His Phe Leu Val Val Asn Met Lys Gly Asn Asp
194           85           90           95
196 Ile Ser Ser Gly Thr Val Leu Ser Asp Tyr Val Gly Ser Gly Pro Pro
197           100          105          110
199 Ser Gly Thr Ser Ile His Arg Tyr Val Trp Leu Val Tyr Glu Gln Glu
200           115          120          125
202 Gln Pro Leu Ser Cys Asp Glu Pro Ile Leu Ser Asn Lys Ser Gly Asp
203           130          135          140
205 Asn Arg Gly Lys Phe Xaa Val Glu Thr Phe Arg Lys Lys Tyr Asn Leu
206 145          150          155          160
208 Gly Ala Pro Val Ala Gly Thr Cys Tyr Gln Ala Glu Trp Asp Asp Tyr
209           165          170          175
211 Val Pro Lys Leu Tyr Glu Gln Leu Ser Gly Lys
212           180          185
214 <210> SEQ ID NO: 4
215 <211> LENGTH: 187
216 <212> TYPE: PRT
217 <213> ORGANISM: Drosophila

```

RAW SEQUENCE LISTING

DATE: 03/16/2001

PATENT APPLICATION: US/09/654,281

TIME: 15:13:59

Input Set : A:\PTO.txt

Output Set: N:\CRF3\03162001\I654281.raw

219 <400> SEQUENCE: 4

```

221 Met Ser Asp Ser Thr Val Cys Phe Ser Lys His Lys Ile Val Pro Asp
222 1 5 10 15
224 Ile Leu Lys Thr Cys Pro Ala Thr Leu Leu Thr Val Thr Tyr Gly Gly
225 20 25 30
227 Gly Gln Val Val Asp Val Gly Gly Glu Leu Thr Pro Thr Gln Val Gln
228 35 40 45
230 Ser Gln Pro Lys Val Lys Trp Asp Ala Asp Pro Asn Ala Phe Tyr Thr
231 50 55 60
233 Leu Leu Leu Thr Asp Pro Asp Ala Pro Ser Arg Lys Glu Pro Lys Phe
234 65 70 75 80
236 Arg Glu Trp His His Trp Leu Val Val Asn Ile Pro Gly Asn Gln Val
237 85 90 95
239 Glu Asn Gly Val Val Leu Thr Glu Tyr Val Gly Ala Gly Pro Pro Gln
240 100 105 110
242 Gly Thr Gly Leu His Arg Tyr Val Phe Ile Val Phe Lys Gln Pro Gln
243 115 120 125
245 Lys Leu Thr Cys Asn Glu Pro Lys Ile Pro Lys Thr Ser Gly Asp Lys
246 130 135 140
248 Arg Ala Asn Phe Ser Thr Ser Lys Phe Met Ser Lys Tyr Lys Leu Gly
249 145 150 155 160
251 Asp Pro Ile Ala Gly Asn Phe Phe Gln Ala Gln Trp Asp Asp Tyr Val
252 165 170 175
254 Pro Lys Leu Tyr Lys Lys Gln Leu Ser Gly Lys Lys
255 180 185

```

257 <210> SEQ ID NO: 5

258 <211> LENGTH: 220

259 <212> TYPE: PRT

260 <213> ORGANISM: C. elegans

262 <400> SEQUENCE: 5

```

264 Met Val Val Leu Val Thr Arg Ser Leu Leu Pro Ala Leu Phe Phe Ala
265 1 5 10 15
267 Ser Arg Ala Pro Phe Ala Ala Ala Thr Thr Ser Ala Arg Phe Gln Arg
268 20 25 30
270 Gly Leu Ala Thr Met Ala Ala Glu Ala Phe Thr Lys His Glu Val Ile
271 35 40 45
273 Pro Asp Val Leu Ala Ser Asn Pro Pro Ser Lys Val Val Ser Val Lys
274 50 55 60
276 Phe Asn Ser Gly Val Glu Ala Asn Leu Gly Asn Val Leu Thr Pro Thr
277 65 70 75 80
279 Gln Val Lys Asp Thr Pro Glu Val Lys Trp Asp Ala Glu Pro Gly Ala
280 85 90 95
282 Leu Tyr Thr Leu Thr Lys Thr Asp Pro Asp Ala Pro Ser Arg Lys Glu
283 100 105 110
285 Pro Thr Tyr Arg Glu Trp His His Trp Leu Val Val Asn Ile Pro Gly
286 115 120 125
288 Asn Asp Ile Ala Lys Gly Asp Thr Leu Ser Glu Tyr Ile Gly Ala Gly
289 130 135 140
291 Pro Pro Lys Thr Gly Leu His Arg Tyr Val Tyr Leu Ile Tyr Lys Gln

```

RAW SEQUENCE LISTING DATE: 03/16/2001
 PATENT APPLICATION: US/09/654,281 TIME: 15:13:59

Input Set : A:\PTO.txt
 Output Set: N:\CRF3\03162001\I654281.raw

```

292 145                      150                      155                      160
294 Ser Gly Arg Ile Glu Asp Ala Glu His Gly Arg Leu Thr Asn Thr Ser
295                      165                      170                      175
297 Gly Asp Lys Arg Gly Gly Trp Lys Ala Ala Asp Phe Val Ala Lys His
298                      180                      185                      190
300 Lys Leu Gly Ala Pro Val Phe Gly Asn Leu Phe Gln Ala Glu Tyr Asp
301                      195                      200                      205
303 Asp Tyr Val Pro Ile Leu Asn Lys Gln Leu Gly Ala
304                      210                      215                      220
306 <210> SEQ ID NO: 6
307 <211> LENGTH: 181
308 <212> TYPE: PRT
309 <213> ORGANISM: Antirrhinum-CEN
311 <400> SEQUENCE: 6
313 Met Ala Ala Lys Val Ser Ser Asp Pro Leu Val Ile Gly Arg Val Ile
314 1                      5                      10                      15
316 Gly Asp Val Val Asp His Phe Thr Ser Thr Val Lys Met Ser Val Ile
317                      20                      25                      30
319 Tyr Asn Ser Asn Asn Ser Ile Lys His Val Tyr Asn Gly His Glu Leu
320                      35                      40                      45
322 Phe Pro Ser Ala Val Thr Ser Thr Pro Arg Val Glu Val His Gly Gly
323                      50                      55                      60
325 Asp Met Arg Ser Phe Phe Thr Leu Ile Met Thr Asp Pro Asp Val Pro
326 65                      70                      75                      80
328 Gly Pro Ser Asp Pro Tyr Leu Arg Glu His Leu His Trp Ile Val Thr
329                      85                      90                      95
331 Asp Ile Pro Gly Thr Thr Asp Ser Ser Phe Gly Lys Glu Val Val Ser
332                      100                      105                      110
334 Tyr Glu Met Pro Arg Pro Asn Ile Gly Ile His Arg Phe Val Phe Leu
335                      115                      120                      125
337 Leu Phe Lys Gln Lys Lys Arg Gly Gln Ala Met Leu Ser Pro Pro Val
338                      130                      135                      140
340 Val Cys Arg Asp Gly Phe Asn Thr Arg Lys Phe Thr Gln Glu Asn Glu
341 145                      150                      155                      160
343 Leu Gly Leu Pro Val Ala Ala Val Phe Phe Asn Cys Gln Arg Glu Thr
344                      165                      170                      175
346 Ala Ala Arg Arg Arg
347                      180
349 <210> SEQ ID NO: 7
350 <211> LENGTH: 176
351 <212> TYPE: PRT
352 <213> ORGANISM: Arabidopsis-TFL1
354 <400> SEQUENCE: 7
356 Met Glu Asn Met Gly Thr Arg Val Ile Glu Pro Leu Ile Met Gly Arg
357 1                      5                      10                      15
359 Val Val Gly Asp Val Leu Asp Phe Phe Thr Pro Thr Thr Lys Met Asn
360                      20                      25                      30
362 Val Ser Tyr Asn Lys Lys Gln Val Asn Gly His Glu Leu Phe Pro Ser
363                      35                      40                      45

```

FYI:

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/654,281

DATE: 03/16/2001
TIME: 15:14:00

Input Set : A:\PTO.txt
Output Set: N:\CRF3\03162001\I654281.raw

L:113 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:116 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:119 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:205 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:471 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10